Name:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_Date:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_Period:\_\_\_\_\_\_\_

**Mendelian Genetics Sickle Cell Anemia Analysis – Part 2**

Thank you to Ms. Glick

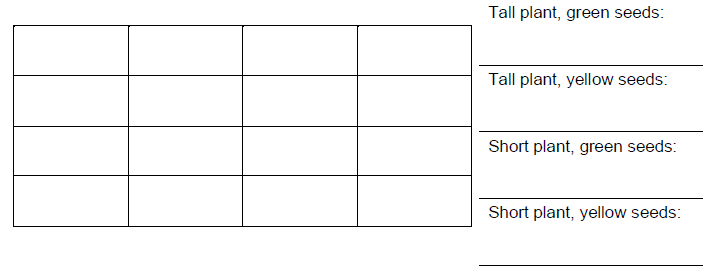
**Multiple Alleles (Blood Types) and Dihybrid Crosses:**

1. In humans, blood type is a result of multiple alleles: A (IA), B (IB), and O (i). A few simple rules of blood type genetics are that

* IA is dominant over i
* IB is dominant over i
* IAIB are codominant.

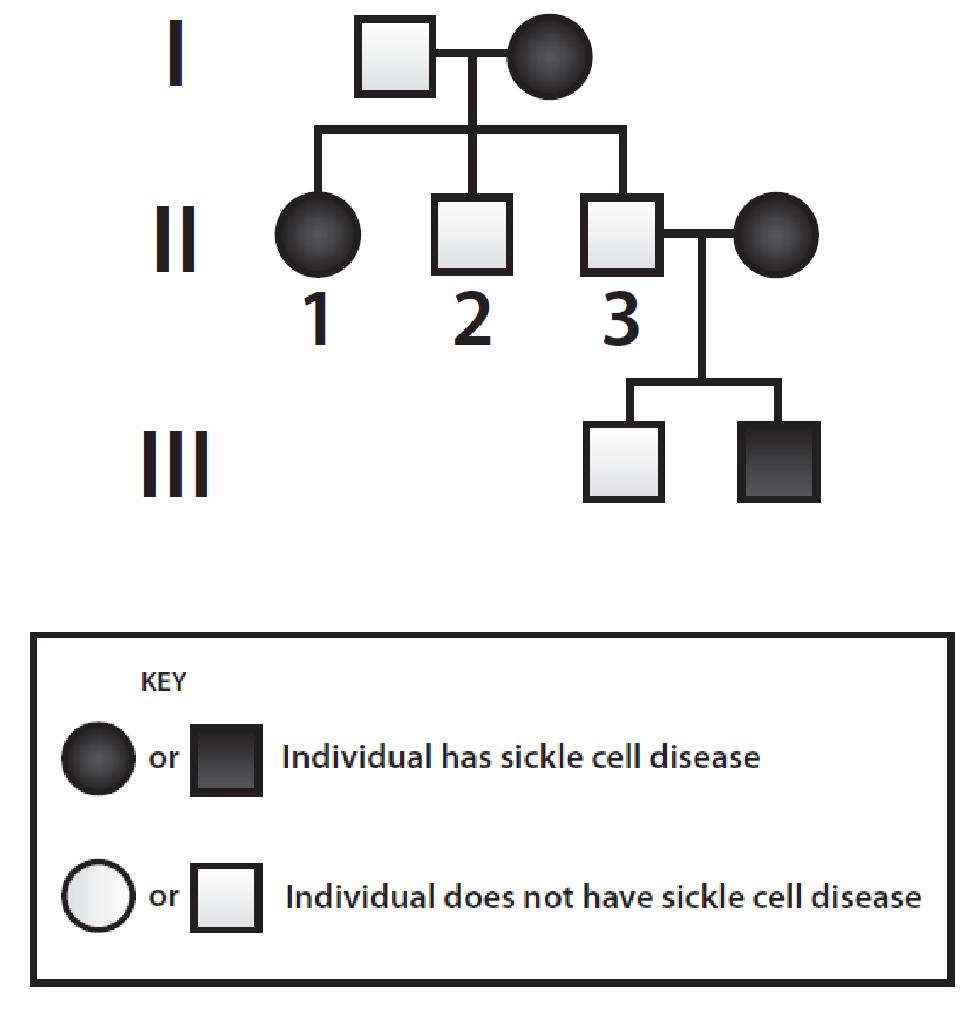
Two parents who are heterozygous for type A blood and have sickle cell trait have children. (Use A to represent the normal hemoglobin allele and S to represent the sickle cell hemoglobin allele). Answer the following questions:

* 1. What is the genotype of the parents?
  2. What are the genetic makeups of all the possible gametes they can produce? (Hint: Use FOIL)
  3. Complete the dihybrid Punnett square to determine the frequency of the different phenotypes in the offspring and list them below as fractions. (Note: Consider blood type and normal vs. sickle cell trait vs. sickle cell disease in the various phenotypes.)



**Pedigrees:**

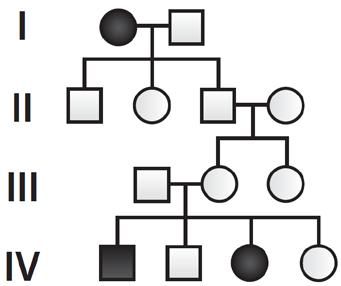
1. The following pedigree traces sickle cell disease through three generations of a family. Use the pedigree to answer the following questions. Individuals who simply carry the sickle cell allele (AS) are unshaded in the pedigree.



* 1. What is the genotype of the father in the first generation?

* 1. What is the genotype of the daughter in the second generation?
  2. What is the genotype of individual 3 in the second generation? How do you know?
  3. If the couple in the second generation has another child, what are the chances the child will have the following?
     1. Sickle cell disease \_\_\_\_\_\_\_\_\_\_
     2. Sickle cell trait \_\_\_\_\_\_\_\_\_\_
     3. Completely normal hemoglobin \_\_\_\_\_\_\_\_\_\_
  4. If the entire family moves to the lowlands of East Africa, four of the five males in the pedigree will have two genetic advantages over the other individuals in the family. Explain the two advantages.

1. The following pedigree traces sickle cell disease through four generations of a family living in New York City. Use the pedigree to answer the following questions.



* 1. What is the genotype of the mother in the first generation?
  2. What are the possible genotypes of the father in the first generation?
  3. What can you say about the genotype of all the children of the couple in the first generation? Explain your answer.
  4. Regarding the answer to the previous question, based on where the family resides, why would this genotype be considered a disadvantage?
  5. What are the genotypes of the parents in the third generation? Explain how you know.
     1. Mother \_\_\_\_\_\_\_\_\_
     2. Father \_\_\_\_\_\_\_\_\_
  6. What is the possible genotype or genotypes of the mother in the second generation?

* 1. If the couple in the third generation has another child, what are the child's chances of the following?
     1. Having sickle cell disease \_\_\_\_\_\_\_\_\_\_
     2. Having sickle cell trait \_\_\_\_\_\_\_\_\_\_
     3. Being homozygous for normal RBCs \_\_\_\_\_\_\_\_\_\_
     4. Being resistant to malaria and not having sickle cell disease \_\_\_\_\_\_\_\_\_\_

**Chi Square Statistical Analysis:**

1. Multiple couples living in a small village in the eastern African lowlands, all of whom are heterozygous for the sickle cell allele, have 500 children among them. Of these children, 139 are homozygous for the normal allele, 279 are heterozygous for the allele, and 82 suffer from sickle cell disease.

You will use a Chi square test to determine if this observed data matches the data you would expect from a Punnett square.

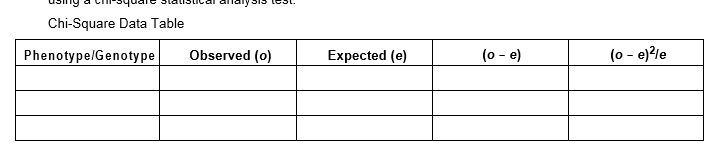
Your null hypothesis is… There is no statistically significant difference between the observed genotype ratios and those expected based on a Punnett square analysis.

For your expected values, first use a Punnett square to determine the expected decimal frequencies of each genotype. Then multiply each of the expected decimal frequencies by 500 (the total number of children) to get the number of children from the population that are expected to have each genotype. These are your “e” values for the Chi square calculation.

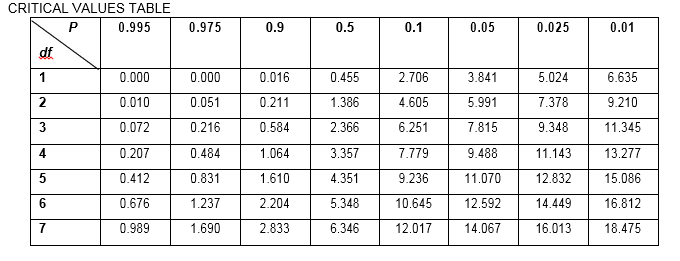
|  |  |
| --- | --- |
|  |  |
|  |  |

|  |  |  |
| --- | --- | --- |
| Genotype | Expected Decimal Frequency | Expected # of Children (out of 500) having this genotype (e values for the Chi square calculation!) |
| AA |  |  |
| AS |  |  |
| SS |  |  |

Now complete your Chi square calculation.



* 1. What is the chi-square value (χ2)? (This is the sum of the numbers in the last column of your data table) \_\_\_\_\_\_\_\_\_\_
  2. Calculate the degrees of freedom (df). \_\_\_\_\_\_\_\_\_\_
  3. Use the degrees of freedom and a p-value of .05 to determine the critical value from the critical values table given below.\_\_\_\_\_\_\_\_\_



* 1. Based on your calculated Chi square value and your critical value, do you reject or fail to reject (i.e. support) your null hypothesis? (Remember: If your Chi square value is higher than your critical value, you reject your null hypothesis. If your Chi square value is lower than your critical value, you fail to reject (i.e. support) your null hypothesis).
  2. What does that mean in the context of this activity?